4
(""
 September 1

# PALM INTRANET

Day : Monday Date: 7/24/2006

Time: 07:53:29

# **Inventor Information for 10/705476**

Inventor Name	City	State/Country
ACHEN, MARC G.	FITZROY	AUSTRALIA
WILKS, ANDREW F.	SOUTH YARRA	AUSTRALIA
STACKER, STEVEN A.	NORTH FITZROY	AUSTRALIA
ALITALO, KARI	ESPOO	FINLAND

Appin info Contents Petition info Atty/Agent info Continuity/Reexam Foreign (
Search Another: Application# Search or Patent# Search
PCT / Search or PG PUBS # Search
Attorney Docket # Search
Bar Code # Search

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# **SCORE Search Results Details for Application** 10705476 and Search Result us-10-705-476-5.rag.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:12:50; Search time 194 Seconds (without alignments)

834.302 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:

2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_8:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\* 9: geneseqp2005s:\*

10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	1963	100.0	354	2	AAW44293	Aaw44293 Human vas
2	1963	100.0	354	2	AAW49036	Aaw49036 Human zve
3	1963	100.0	354	2	AAW53241	Aaw53241 Homo sapi
4	1963	100.0	354	3	AAB10649	Aab10649 Human VEG
5	1963	100.0	354	3	AAY70750	Aay70750 Human pre
6	1963	100.0	354	3	AAY70983	Aay70983 Human vas
7	1963	100.0	354	3	AAB29049	Aab29049 Human VEG
8	1963	100.0	354	4	AAB37606	Aab37606 Human VEG
9	1963	100.0	354	4	AAY97573	Aay97573 Human VEG
10	1963	100.0	354	4	AAU08441	Aau08441 Polypepti
11	1963	100.0	354	5	ABG33055	Abg33055 Human vas
12	1963	100.0	354	5	ABG32 04 6	Abg32046 Human Flt
13	1963	100.0	354	6	ABB84 623	Abb84623 Human VEG
14	1963	100.0	354	7	ADD08950	Add08950 Human VEG
15	1963	100.0	354	7	ADN95941	Adn95941 Human VEG
16	1963	100.0	354	8	ADQ20886	Adq20886 Human sof
17	1963	100.0	354	8	ADO71602	Ado71602 A human v
18	1963	100.0	354	8	ADR31436	Adr31436 Human vas
19	1963	100.0	354	9	ADW80993	Adw80993 Human vas
20	1963	100.0	354	9	ADX69284	Adx69284 Human VEG
21	1963	100.0	354	9	ADZ00442	Adz00442 VEGF-D. 6
22	1963	100.0	354	9	ADZ79971	Adz79971 Human vas
23	1963	100.0	354	9	AEC08002	Aec08002 Human VEG
24	1963	100.0	354	9	AEC78160	Aec78160 Human VEG
25	1963	100.0	354	9	AED26685	Aed26685 Human VEG
26	1963	100.0	354	9	AED34383	Aed34383 Human vas
27	1963	100.0	354	9	AED12196	Aed12196 Vascular
28	1963	100.0	354	9	AED12194	Aed12194 Vascular
29	1963	100.0	354	10	AEF51599	Aef51599 VEGF-D, S
30	1926	98.1	354	4	AAB70685	Aab70685 Human vas
31	1917	97.7	620	2	AAW14994	Aaw14994 Human c-F
32	1804	91.9	325	2	AAW53240	Aaw53240 Homo sapi
33	1804	91.9	325	4	AAY97572	Aay97572 Human VEG
34	1675	85.3	358	2	AAW44295	Aaw44295 Mouse vas
35	1675	85.3	358	2	AAW53242	Aaw53242 Mus muscu
36	1675	85.3	358	5	AAM47930	Aam47930 Mouse VEG
37	1675	85.3	358	10	AEF51601	Aef51601 VEGF-D1 1
38	1671	85.1	358	2	AAW14992	Aaw14992 Murine c-
39	1608.5	81.9	337	2	AAY08286	Aay08286 Human gro
40	1525	77.7			ABG73 779	Abg73779 Human NVR
41	1522	77.5	321	2	AAW53243	Aaw53243 Mus muscu
42	1522	77.5	321	5	AAM47931	Aam47931 Mouse VEG
43	1522	77.5	321	10	AEF51603	Aef51603 VEGF-D2 s
44	1517.5	77.3	326	2	AAW44296	Aaw44296 Rat vascu
45	834.5	42.5	178	2	AAY08287	Aay08287 Human gro

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RESULT 1
    AAW44293 standard; protein; 354 AA.
XX
AC
    AAW44293;
XX
     22-JUN-1998 (first entry)
DT
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### **SCORE Search Results Details for Application** 10705476 and Search Result us-10-705-476-5.ra

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:21:40; Search time 49 Seconds (without alignments)

632.364 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters:

650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

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3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\* 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*

5: /EMC Celerra SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Length	DB	ID	Description		
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2	1963	100.0	354	2	US-09-296-275-5	Sequence !	
3	1963	100.0	354	2	US-09-375-248-6	Sequence	
4	1963	100.0	354	2	US-09-468-647A-109	Sequence	
5	1963	100.0	354	2	US-09-169-079-22	Sequence	
6	1963	100.0	354	2	US-09-214-982-1	Sequence	
7	1963	100.0	354	2	US-09-427-657-4	Sequence 4	
8	1963	100.0	354	2	US-09-795-006A-119	Sequence	119, App
9	1963	100.0	354	3	US-09-765-534B-22	Sequence	22, Appl
10	1963	100.0	362	2	US-09-949-016-11286	Sequence	
11	1804	91.9	325	2	US-08-915-795-3	Sequence	
12	1804	91.9	325	2	US-09-296-275-3	Sequence :	3, Appli
13	1675	85.3	358	2	US-08-915-795-8	Sequence	8, Appli
14	1675	85.3	358	2	US-09-847-524-2	Sequence :	2, Appli
15	1675	85.3	358	2	US-09-296-275-8	Sequence	8, Appli
16	1675	85.3	358	2	US-09-438-046-15	Sequence	15, Appl
17	1522	77.5	321	2	US-08-915-795-9	Sequence	9, Appli
18	1522	77.5	321	2	US-09-847-524-4	Sequence	4, Appli
19	1522	77.5	321	2	US-09-296-275-9	Sequence	9, Appli
20	1087	55.4	197	2	US-09-431-888-8	Sequence	8, Appli
21	704.5	35.9	419	1	US-08-999-811-2	Sequence	2, Appli
22	704.5	35.9	419	2	US-09-042-105-2	Sequence :	2, Appli
23	704.5	35.9	419	2	US-09-042-105-18	Sequence	18, Appl
24	704.5	35.9	419	2	US-08-795-430-8	Sequence	8, Appli
25	704.5	35.9	419	2	US-08-510-133A-35	Sequence	35, Appl
26	704.5	35.9	419	2	US-09-355-700-8	Sequence	8, Appli
27	704.5	35.9	419	2	US-08-601-132-33	Sequence	33, Appl
28	704.5	35.9	419	2	US-08-465-968-2	Sequence	2, Appli
29	704.5	35.9	419	2	US-08-671-573B-33	Sequence	
30	704.5	35.9	419	2	US-09-438-046-14	Sequence	
31	704.5	35.9	419	2	US-09-631-092B-33	Sequence	33, Appl
32	704.5	35.9	419	2	US-10-084-488-2	Sequence	
33	704.5	35.9	419	2	US-10-084-488-18	Sequence	
34	704.5	35.9	419	2	US-09-375-248-4	Sequence	4, Appli
35	704.5	35.9	419	2	US-09-468-647A-108	Sequence	
36	704.5	35.9	419	2	US-09-534-376A-8	Sequence	=
37	704.5	35.9	419	2	US-09-169-079-21	Sequence	
38	704.5	35.9	419	2	US-09-427-657-2	Sequence	
39	704.5	35.9	419	2	US-09-795-006A-22	Sequence	
40	704.5	35.9	419	2	US-08-743-868-2	Sequence	
41	704.5	35.9	419	2	US-09-499-468-2	Sequence	
42	704.5	35.9	419	2	US-09-219-442-2	Sequence	
43	701.5	35.9	419	3	US-09-765-534B-21	Sequence	
44	701.5	35.9	419	5	PCT-US96-09001-2	Sequence	
45	699.5	35.6	419	2	US-09-214-982-29	Sequence	
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RESULT 1
US-08-915-795-5
; Sequence 5, Application US/08915795
; Patent No. 6235713
; GENERAL INFORMATION:
   APPLICANT: Marc G. ACHEN
    APPLICANT: Andrew F. WILKS
    APPLICANT: Steven A. STACKER
    APPLICANT: Kari ALITALO
    TITLE OF INVENTION: GROWTH FACTOR
    NUMBER OF SEQUENCES: 11
    CORRESPONDENCE ADDRESS:
```

### **SCORE Search Results Details for Application** 10705476 and Search Result us-10-705-476-5.rapbm.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:33:36; Search time 185 Seconds (without alignments)

886.368 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

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2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

옿 Query

Score Match Length DB ID

Description

1	1963	100.0	354	3	US-09-956-095-2	Sequence	2, Appli
2	1963	100.0	354	3	US-09-219-345A-11		11, Appl
3	1963	100.0	354	3	US-09-795-006A-119		119, App
4	1963	100.0	354	3	US-09-375-248-6		6, Appli
5	1963	100.0	354	3	US-09-765-534B-22	_	22, Appl
6	1963	100.0	354	4	US-10-262-538-26		26, Appl
7	1963	100.0	354	4	US-10-274-953-5		5, Appli
8	1963	100.0	354	4	US-10-161-694-5	_	5, Appli
9	1963	100.0	354	4	US-10-661-740-6	_	6, Appli
10	1963	100.0	354	4	US-10-705-476-5	Sequence	5, Appli
11	1963	100.0	354	4	US-10-774-802-22		22, Appl
12	1963	100.0	354	4	US-10-669-176-26		26, Appl
13	1963	100.0	354	5	US-10-772-927A-18	_	18, Appl
14	1963	100.0	354	5	US-10-723-860-3706	Sequence	3706, Ap
15	1963	100.0	354	5	US-10-868-577A-4		4, Appli
16	1963	100.0	354	5	US-10-868-549-4	_	4, Appli
17	1963	100.0	354	5	US-10-978-107-1		1, Appli
18	1963	100.0	354	5	US-10-924-025A-109	Sequence	109, App
19	1963	100.0	354	5	US-10-756-149-5641	Sequence	5641, Ap
20	1963	100.0	354	5	US-10-627-631-2	Sequence	2, Appli
21	1963	100.0	354	5	US-10-921-793-70	Sequence	70, Appl
22	1963	100.0	354	5	US-10-931-198-70	Sequence	70, Appl
23	1963	100.0	354	5	US-10-942-042-70	Sequence	70, Appl
24	1963	100.0	354	6	US-11-064-769-4	Sequence	4, Appli
25	1963	100.0	354	6	US-11-090-439-60	Sequence	60, Appl
26	1963	100.0	354	6	US-11-090-439-62	Sequence	62, Appl
27	1963	100.0	354	6	US-11-064-774A-119	Sequence	119, App
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31	1963	100.0	354	6	US-11-076-427A-8	Sequence	8, Appli
32	1963	100.0	354	6	US-11-075-047A-87	Sequence	87, Appl
33	1956	99.6	362	4	US-10-139-876-4	Sequence	4, Appli
34	1926	98.1	354	4	US-10-174-930-1	•	1, Appli
35	1804	91.9	325	4	US-10-274-953-3	Sequence	3, Appli
36	1804	91.9	325	4	US-10-161-694-3	Sequence	3, Appli
37	1804	91.9	325	4	US-10-705-476-3		3, Appli
38	1675	85.3	358	3	US-09-852-209A-13		13, Appl
39	1675	85.3	358	3	US-09-847-524-2	Sequence	2, Appli
40	1675	85.3	358	4	US-10-139-876-2	•	2, Appli
41	1675	85.3	358	4	US-10-131-600-13		13, Appl
42	1675	85.3	358	4	US-10-274-953-8		8, Appli
43	1675	85.3	358	4	US-10-161-694-8	<del>-</del>	8, Appli
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RESULT 1
US-09-956-095-2
; Sequence 2, Application US/09956095
; Patent No. US20020102260A1
; GENERAL INFORMATION:
; APPLICANT: ACHEN, Marc G.
; APPLICANT: STACKER, Steven A.
; TITLE OF INVENTION: METHODS FOR TREATING NEOPLASTIC DISEASE CHARACTERIZED BY
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR D EXPRESSION, FOR SCREENING
; TITLE OF INVENTION: FOR NEOPLASTIC DISEASE OR METASTATIC RISK AND FOR MAINTAINING
; TITLE OF INVENTION: VASCULARIZATION OF TISSUE
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### **SCORE Search Results Details for Application** 10705476 and Search Result us-10-705-476-5.rapbn.

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GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:33:55; Search time 21 Seconds (without alignments)

452.312 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score:

1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

112942 seqs, 26832045 residues

Total number of hits satisfying chosen parameters:

112942

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA\_New:\*

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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*

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4: /EMC Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*

6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	1963	100.0	354	6	US-10-505-928-866	Sequence 866, App
2	704.5	35.9	419	6	US-10-505-928-436	Sequence 436, App
3	704.5	35.9	419	6	US-10-505-928-864	Sequence 864, App
4	695.5	35.4	419	7	US-11-346-806-3	Sequence 3, Appli
5	169.5	8.6	147	7	US-11-346-806-4	Sequence 4, Appli
6	160.5	8.2	149	7	US-11-346-806-5	Sequence 5, Appli
7	160.5	8.2	170	6	US-10-505-928-584	Sequence 584, App
8	147	7.5	345	7	US-11-289-102-249	Sequence 249, App
9	115.5	5.9	426	6	US-10-449-902-54143	Sequence 54143, A
10	114.5	5.8	1093	6	US-10-449-902-41338	Sequence 41338, A
11	114.5	5.8	1287	6	US-10-505-928-341	Sequence 341, App
12	113	5.8	756	6	US-10-449-902-44363	Sequence 44363, A
13	112.5	5.7	259	7	US-11-217-997-34	Sequence 34, Appl
14	112.5	5.7	575	7	US-11-217-997-32	Sequence 32, Appl
15	112.5	5.7	1398	7	US-11-217-997-4	Sequence 4, Appli
16	112.5	5.7	1403	7	US-11-217-997-12	Sequence 12, Appl
17	112.5	5.7	1404	7	US-11-217-997-2	Sequence 2, Appli
18	112.5	5.7	1547	7	US-11-217-997-22	Sequence 22, Appl
19	112.5	5.7	1577	7	US-11-217-997-16	Sequence 16, Appl
20	112.5	5.7	1577	7	US-11-217-997-20	Sequence 20, Appl
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22	112.5	5.7	1620	7	US-11-217-997-42	Sequence 42, Appl
23	112.5	5.7	1653	7	US-11-217-997-40	Sequence 40, Appl
24	111	5.7	2003	7	US-11-264-243-8	Sequence 8, Appli
25	108.5	5.5	342	7	US-11-038-753-1	Sequence 1, Appli
26	108	5.5	685	7	US-11-293-697-3546	Sequence 3546, Ap
27	105.5	5.4	1418	7	US-11-217-997-38	Sequence 38, Appl
28	104.5	5.3	909 469	6 7	US-10-449-902-44686	Sequence 44686, A
29	103.5 103.5	5.3 5.3	469	7	US-11-246-999-41 US-11-246-999-30	Sequence 41, Appl Sequence 30, Appl
30 31	103.5	5.3	567	7	US-11-246-999-50	Sequence 50, Appl
32	103.5	5.2	2556	7	US-11-264-243-6	Sequence 6, Appli
33	101.5	5.2	1218	7	US-11-204-243-0 US-11-178-724-21	Sequence 21, Appl
34	101.5	5.2	1218	7	US-11-071-796A-20	Sequence 20, Appl
	101.5	5.1	472	7	US-11-217-997-26	Sequence 26, Appl
36	101	5.1	2556	7	US-11-071-796A-22	Sequence 22, Appl
37	100.5	5.1	364	6	US-10-449-902-36200	Sequence 36200, A
38	100.5	5.1	1198	7	US-11-217-997-14	Sequence 14, Appl
39	100.5					Sequence 6, Appli
40	100	5.1	563	6	US-10-449-902-47820	Sequence 47820, A
41	100	5.1	563	6	US-10-449-902-55504	Sequence 55504, A
42	99.5	5.1	177	7	US-11-223-945-37	Sequence 37, Appl
43	98	5.0	314	6	US-10-953-349-10973	Sequence 10973, A
44	98	5.0	419	6	US-10-953-349-10972	Sequence 10972, A
45	98	5.0	422	6	US-10-953-349-10971	Sequence 10971, A

```
RESULT 1
US-10-505-928-866
; Sequence 866, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
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# SCORE Search Results Details for Application 10705476 and Search Result us-10-705-476-5.ra

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10705476 and Search Result us-10-70 5.rapm.

start

Go Back to pre

```
GenCore version 5.1.9
                 Copyright (c) 1993 - 2006 Biocceleration Ltd.
OM protein - protein search, using sw model
               July 5, 2006, 22:22:25; Search time 604 Seconds
Run on:
                                          (without alignments)
                                          894.938 Million cell updates/sec
Title:
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Perfect score: 1963
               1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354
Sequence:
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
               8366291 seqs, 1526956180 residues
Searched:
Total number of hits satisfying chosen parameters:
                                                       8366291
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                Maximum Match 100%
                Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		*				
Result		Query				
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				<b>-</b> -		
1	1963	100.0	354	1	PCT-US00-14925-22	Sequence 22, Appl
2	1963	100.0	354	1	PCT-US03-36644-12	Sequence 12, Appl
3	1963	100.0	354	1	PCT-US03-38193-3706	Sequence 3706, Ap
4	1963	100.0	354	1	PCT-US05-10109-60	Sequence 60, Appl
5	1963	100.0	354	1	PCT-US05-10109-62	Sequence 62, Appl
6	1963	100.0	354	1	PCT-US05-47288-49	Sequence 49, Appl
7	1963	100.0	354	1	PCT-US97-14696-5	Sequence 5, Appli
8	1963	100.0	354	1	PCT-US99-06133-6	Sequence 6, Appli
9	1963	100.0	354	17	US-08-759-657-2	Sequence 2, Appli
10	1963	100.0	354	19	US-08-933-455-2	Sequence 2, Appli
11	1963	100.0	354	22	US-09-219-345A-11	Sequence 11, Appl
12	1963	100.0	354	22	US-09-219-345B-10	Sequence 10, Appl
13	1963	100.0	354	27	US-09-791-537-91625	Sequence 91625, A
14	1963	100.0	354	29	US-09-956-095-2	Sequence 2, Appli
15	1963	100.0	354	31	US-10-161-694-5	Sequence 5, Appli
16	1963	100.0	354	32	US-10-262-538-26	Sequence 26, Appl
17	1963	100.0	354	32	US-10-262-538A-26	Sequence 26, Appl
18	1963	100.0	354	32	US-10-274-953-5	Sequence 5, Appli

# **SCORE Search Results Details for Application** 10705476 and Search Result us-10-705-476-5.rapn.

Score Home Page

Retrieve Application

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**SCORE System** Overview

SCORE <u>FAQ</u>

Comments / Suggestions

This page gives you Search Results detail for the Application 10705476 and Search Result us-10-705-476-5.rapn.

<u>start</u>

Go Back to previous page

```
GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
```

OM protein - protein search, using sw model

Run on:

July 5, 2006, 22:23:20; Search time 24 Seconds (without alignments)

592.798 Million cell updates/sec

Title:

US-10-705-476-5

Perfect score: 1963

Sequence:

1 MYREWVVVNVFMMLYVQLVQ......HCRFPKEKRAAQGPHSRKNP 354

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

179241 seqs, 40189672 residues

Total number of hits satisfying chosen parameters:

179241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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Pending\_Patents\_AA\_New: \*

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3: /EMC\_Celerra\_SIDS3/ptodata/1/paa/US07\_NEW\_COMB.pep:\*

4: /EMC Celerra\_SIDS3/ptodata/1/paa/US08\_NEW\_COMB.pep:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

Result

Query

No.	Score	Match	Length	DB	ID	Description
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1	1963	100.0	354	8	US-60-808-106-52	Sequence 52, Appl
2	704.5	35.9	419	5	US-09-499-468-2	Sequence 2, Appli
3	704.5	35.9 35.9	419	7	US-11-429-373-570	Sequence 570, App Sequence 571, App
4	704.5		419	7	US-11-429-373-571	<del>-</del>
5	704.5	35.9	419	7	US-11-429-373-573	Sequence 573, App
6	704.5	35.9	419	7 7	US-11-429-373-574	Sequence 574, App
7	704.5	35.9	419		US-11-429-374-570	Sequence 570, App
8	704.5	35.9	419	7	US-11-429-374-571	Sequence 571, App
9	704.5	35.9	419	7	US-11-429-374-573 US-11-429-374-574	Sequence 573, App
10	704.5	35.9	419	7		Sequence 574, App
11	704.5	35.9	419	7 7	US-11-429-276-570	Sequence 570, App
12	704.5	35.9	419		US-11-429-276-571	Sequence 571, App Sequence 573, App
13	704.5	35.9	419	7 7	US-11-429-276-573	
14	704.5	35.9	419		US-11-429-276-574	Sequence 574, App
15	704.5	35.9	419	8	US-60-808-106-51	Sequence 51, Appl
16	664.5	33.9	350	5 7	US-09-499-468-4	Sequence 4, Appli
17	421.5	21.5	734	7	US-11-429-373-354	Sequence 354, App
18	421.5	21.5	734	7	US-11-429-373-357	Sequence 357, App
19	421.5	21.5	734	7	US-11-429-374-354	Sequence 354, App Sequence 357, App
20	421.5	21.5	734		US-11-429-374-357	_
21	421.5	21.5	734	7	US-11-429-276-354	Sequence 354, App
22	421.5	21.5	734	7	US-11-429-276-357	Sequence 357, App
23	413	21.0	734	7	US-11-429-373-355	Sequence 355, App
24	413	21.0	734	7	US-11-429-373-358	Sequence 358, App
25	413	21.0	734	7	US-11-429-374-355	Sequence 355, App
26	413	21.0	734	7	US-11-429-374-358	Sequence 358, App
27	413	21.0	73.4	7	US-11-429-276-355	Sequence 355, App
28	413	21.0	734	7	US-11-429-276-358	Sequence 358, App
29	204	10.4	165	7	US-11-414-782-8	Sequence 8, Appli
30	204	10.4	165	8	US-60-808-106-4	Sequence 4, Appli
31	204	10.4	165	8	US-60-808-106-22	Sequence 22, Appl
32	204	10.4	191	6	US-10-207-655A-51	Sequence 51, Appl
33	204	10.4	191	7	US-11-441-790-1	Sequence 1, Appli
34	204	10.4	191	7	US-11-207-655-51	Sequence 51, Appl
35	204	10.4	191	8	US-60-808-106-2	Sequence 2, Appli
36	204	10.4	191	8	US-60-808-106-21	Sequence 21, Appl
37	203	10.3	190	8	US-60-808-106-33	Sequence 33, Appl
38	201	10.2	183	7	US-11-414-782-7	Sequence 7, Appli
39	201	10.2	183	8	US-60-808-106-15	Sequence 15, Appl
40	201	10.2	209	8	US-60-808-106-14	Sequence 14, Appl
41	200.5	10.2	206	7	US-11-414-782-5	Sequence 5, Appli
42	200.5	10.2	206	8	US-60-808-106-19	Sequence 19, Appl
43	200.5	10.2	232	5	US-09-499-468-7	Sequence 7, Appli
44	200.5	10.2	232	8	US-60-808-106-18	Sequence 18, Appl
45	200	10.2	164	8	US-60-808-106-25	Sequence 25, Appl

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RESULT 1
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; Sequence 52, Application US/60808106
; GENERAL INFORMATION:
; APPLICANT: Szkudlinski, Mariusz W.
; APPLICANT: Weintraub, Bruce
; TITLE OF INVENTION: VEGF Analogs and Methods of Use
; FILE REFERENCE: TROP-005/01US
; CURRENT APPLICATION NUMBER: US/60/808,106
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### **SCORE Search Results Deta**

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Sugg

This page gives you Search Results detail for the Application 10705476 and Search Result us-10-70 start

> GenCore version 5.1.9 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM protein - protein search, using sw model

July 5, 2006, 22:16:40; Search time 41 Seconds

(without alignments)

830.750 Million cell updates/sec

Title: US-10-705-476-5

Perfect score: 1963

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Scoring table: BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80:\*

> 1: pir1:\* 2: pir2:\*

> 3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		₹				
Result		Query				
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1	704.5	35.9	419	2	S69207	vascular endothell
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3	200	10.2	190	2	B40080	vascular endotheli
4	198	10.1	190	2	S52130	vascular endotheli
5	198	10.1	190	2	B44881	vascular endotheli
6	198	10.1	214	2	A44881	vascular endotheli
7	194	9.9	190	2	A35987	glioma-derived vas
8	181.5	9.2	1700	2	S08167	Balbiani ring 3 pr

9	176.5	9.0	188	2	JC4680	vascular endotheli
10	167.5	8.5	146	2	S57956	ovine vascular end
11	166.5	8.5	120	2	A33787	vascular endotheli
12	164	8.4	148	2	D49530	16K vascular endot
13	161	8.2	245	1	TVCTSS	platelet-derived g
14	160.5	8.2	149	2	A41236	placental growth f
15	158	8.0	158	2	A56125	placental growth f
16	147.5	7.5	207	2	JC4679	vascular endotheli
17	145	. 7.4	133	2	B49530	vascular endotheli
18	145	7.4	241	1	PFHUG2	platelet-derived g
19	139.5	7.1	1187	2	T18355	hypothetical prote
20	135	6.9	241 <sup>-</sup>	1	PFMSGB	platelet-derived g
21	133.5	6.8	225	2	S25097	platelet-derived g
22	130.5	6.6	370	2	JC7592	spinal cord-derive
23	128	6.5	748	2	S66129	disintegrin (EC 3.
24	125.5	6.4	196	2	B28964	platelet-derived g
25	125.5	6.4	211	1	PFHUG1	platelet-derived g
26	125	6.4	2946	2	T15840	hypothetical prote
27	123.5	6.3	370	2	JC7591	spinal cord-derive
28	122	6.2	226	1	TVMVSS	PDGF-related trans
29	120.5	6.1	160	2	JQ0542	185K secretory pro
30	120	6.1	200	2	<b>I51551</b>	platelet-derived g
31	120	6.1	215	2	S08220	platelet-derived g
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34	118	6.0	965	2	S62935	hypothetical prote
35	117.5	6.0	370	2	JC7998	platelet-derived g
36	116	5.9	1548	2	S34583	serine proteinase
37	115.5	5.9	1964	2	T09059	notch4 - mouse
38	114.5	5.8	1287	2	A41685	SIL protein - huma
39	114.5	5.8	5376	2	T42215	zonadhesin - mouse
40	113	5.8	197	2	S25096	platelet-derived g
41	113	5.8	846	2	A30889	integrin beta chai
42	112.5	5.7	2195	2	T34264	hypothetical prote
43	112	5.7	3635	2	T10053	laminin alpha 5 ch
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C; Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C; Accession: S69207; S61795; S71443; S69208; G02659
R; Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela
EMBO J. 15, 1751, 1996
A; Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand
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A; Accession: S69207
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-419
A;Cross-references: UNIPROT:P49767; UNIPARC:UPI0000001C2A; EMBL:X94216; NID:g1177488;
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A; Note: only a part of the translation is shown
A; Note: this is a revision to the sequence from reference S61795
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